

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/508,965  
Source: IFWO  
Date Processed by STIC: 11/28/06

# **ENTERED**



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/508,965

DATE: 11/28/2006

TIME: 13:00:13

Input Set : A:\051530-5007-US Sequence Listing.txt  
 Output Set: N:\CRF4\11282006\J508965.raw

3 <110> APPLICANT: Transmolecular, Inc.  
 4 GONDA, Matthew A  
 5 GREENWOOD, John D  
 7 <120> TITLE OF INVENTION: Recombinant Expression Vectors for Functional Nav1.9 Sodium  
 Channels  
 9 <130> FILE REFERENCE: 51530-5007-US  
 11 <140> CURRENT APPLICATION NUMBER: US 10/508,965  
 C--> 12 <141> CURRENT FILING DATE: 2004-09-23  
 14 <150> PRIOR APPLICATION NUMBER: PCT/US03/08611  
 15 <151> PRIOR FILING DATE: 2003-03-20  
 17 <150> PRIOR APPLICATION NUMBER: US 60/365,550  
 18 <151> PRIOR FILING DATE: 2002-03-20  
 20 <160> NUMBER OF SEQ ID NOS: 35  
 22 <170> SOFTWARE: PatentIn version 3.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 5905  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Rattus norvegicus  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: CDS  
 31 <222> LOCATION: (52)..(5349)  
 34 <400> SEQUENCE: 1  
 35 tctggagcca tacggtgccc tgatcctctg taccaggaag acagggtgaa g atg gag 57  
 36 1  
 37 Met Glu  
 39 gag agg tac tac ccg gtg atc ttc ccg gac gag ccg aat ttc cgc ccc 105  
 40 Glu Arg Tyr Tyr Pro Val Ile Phe Pro Asp Glu Arg Asn Phe Arg Pro  
 41 5 10 15  
 43 ttc act tcc gac tct ctg gct gcc ata gag aag ccg att gct atc caa 153  
 44 Phe Thr Ser Asp Ser Leu Ala Ala Ile Glu Lys Arg Ile Ala Ile Gln  
 45 20 25 30  
 47 aag gag agg aag tcc aaa gac aag gcg gca gct gag ccc cag cct 201  
 48 Lys Glu Arg Lys Lys Ser Lys Asp Lys Ala Ala Ala Glu Pro Gln Pro  
 49 35 40 45 50  
 51 cgg cct cag ctt gac cta aag gcc tcc agg aag tta cct aag ctt tat 249  
 52 Arg Pro Gln Leu Asp Leu Lys Ala Ser Arg Lys Leu Pro Lys Leu Tyr  
 53 55 60 65  
 55 ggt gac att ccc cct gag ctt gta gcg aag cct ctg gaa gac ctg gac 297  
 56 Gly Asp Ile Pro Pro Glu Leu Val Ala Lys Pro Leu Glu Asp Leu Asp  
 57 70 75 80  
 59 cca ttc tac aaa gac cat aag aca ttc atg gtg ttg aac aag aag aga 345  
 60 Pro Phe Tyr Lys Asp His Lys Thr Phe Met Val Leu Asn Lys Lys Arg  
 61 85 90 95  
 63 aca att tat cgc ttc agc gcc aag ccg gcc ttg ttc att ctg ggg cct 393

*See P'6*

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64	Thr	Ile	Tyr	Arg	Phe	Ser	Ala	Lys	Arg	Ala	Leu	Phe	Ile	Leu	Gly	Pro	
65	100				105							110					
67	ttt	aat	ccc	ctc	aga	agc	tta	atg	att	cgt	atc	tct	gtc	cat	tca	gtc	441
68	Phe	Asn	Pro	Leu	Arg	Ser	Leu	Met	Ile	Arg	Ile	Ser	Val	His	Ser	Val	
69	115						120				125					130	
71	ttt	agc	atg	tcc	atc	atc	tgc	acg	gtg	atc	atc	aac	tgt	atg	tcc	atg	489
72	Phe	Ser	Met	Phe	Ile	Ile	Cys	Thr	Val	Ile	Ile	Asn	Cys	Met	Phe	Met	
73							135				140					145	
75	gcg	aat	tct	atg	gag	aga	agt	tcc	gac	aac	gac	att	ccc	gaa	tac	gtc	537
76	Ala	Asn	Ser	Met	Glu	Arg	Ser	Phe	Asp	Asn	Asp	Ile	Pro	Glu	Tyr	Val	
77							150			155					160		
79	ttc	att	ggg	att	tat	att	tta	gaa	gct	gtg	att	aaa	ata	ttg	gca	aga	585
80	Phe	Ile	Gly	Ile	Tyr	Ile	Leu	Glu	Ala	Val	Ile	Lys	Ile	Leu	Ala	Arg	
81							165			170					175		
83	ggc	ttc	att	gtg	gat	gag	ttt	tcc	tcc	ctc	cga	gat	ccg	tgg	aac	tgg	633
84	Gly	Phe	Ile	Val	Asp	Glu	Phe	Ser	Phe	Leu	Arg	Asp	Pro	Trp	Asn	Trp	
85							180			185					190		
87	ctg	gac	tcc	att	gtc	att	gga	aca	gca	atc	gca	act	tgt	ttt	ccg	ggc	681
88	Leu	Asp	Phe	Ile	Val	Ile	Gly	Thr	Ala	Ile	Ala	Thr	Cys	Phe	Pro	Gly	
89	195						200			205					210		
91	agc	caa	gtc	aat	ctt	tca	gct	ctt	cgt	acc	ttc	cga	gtg	ttc	aga	gct	729
92	Ser	Gln	Val	Asn	Leu	Ser	Ala	Leu	Arg	Thr	Phe	Arg	Val	Phe	Arg	Ala	
93							215			220					225		
95	ctg	aag	gcg	att	tca	gtt	atc	tca	ggt	ctg	aag	gtc	atc	gta	ggt	gcc	777
96	Leu	Lys	Ala	Ile	Ser	Val	Ile	Ser	Gly	Leu	Lys	Val	Ile	Val	Gly	Ala	
97							230			235					240		
99	ctg	ctg	ctg	gtg	aag	aag	ctg	gta	gac	gtg	atg	gtc	ctc	act	ctc		825
100	Leu	Leu	Arg	Ser	Val	Lys	Lys	Leu	Val	Asp	Val	Met	Val	Leu	Thr	Leu	
101							245			250					255		
103	ttc	tgc	ctc	agc	atc	ttt	gcc	ctg	gtc	ggt	cag	cag	ctg	ttc	atg	gga	873
104	Phe	Cys	Leu	Ser	Ile	Phe	Ala	Leu	Val	Gly	Gln	Gln	Leu	Phe	Met	Gly	
105							260			265					270		
107	att	ctg	aac	cag	aag	tgt	att	aag	cac	aac	tgt	ggc	ccc	aac	cct	gca	921
108	Ile	Leu	Asn	Gln	Lys	Cys	Ile	Lys	His	Asn	Cys	Gly	Pro	Asn	Pro	Ala	
109	275						280			285					290		
111	tcc	aac	aag	gat	tgc	ttt	gaa	aag	gaa	aaa	gat	agc	gaa	gac	ttc	ata	969
112	Ser	Asn	Lys	Asp	Cys	Phe	Glu	Lys	Glu	Lys	Asp	Ser	Glu	Asp	Phe	Ile	
113							295			300					305		
115	atg	tgt	ggt	acc	tgg	ctc	ggc	agc	aga	ccc	tgt	ccc	aat	ggt	tct	acg	1017
116	Met	Cys	Gly	Thr	Trp	Leu	Gly	Ser	Arg	Pro	Cys	Pro	Asn	Gly	Ser	Thr	
117							310			315					320		
119	tgc	gat	aaa	acc	aca	ttg	aac	cca	gac	aat	aat	tat	aca	aag	ttt	gac	1065
120	Cys	Asp	Lys	Thr	Thr	Leu	Asn	Pro	Asp	Asn	Asn	Tyr	Thr	Lys	Phe	Asp	
121							325			330					335		
123	aac	ttt	ggc	tgg	tcc	ttt	ctc	gcc	atg	tcc	cg	gtt	atg	act	caa	gac	1113
124	Asn	Phe	Gly	Trp	Ser	Phe	Leu	Ala	Met	Phe	Arg	Val	Met	Thr	Gln	Asp	
125							340			345					350		
127	tcc	tgg	gag	agg	ctt	tac	cga	cag	atc	ctg	cg	acc	tct	ggg	atc	tac	1161
128	Ser	Trp	Glu	Arg	Leu	Tyr	Arg	Gln	Ile	Leu	Arg	Thr	Ser	Gly	Ile	Tyr	

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129	355	360	365	370														
131	ttt	gtc	ttc	ttc	gtg	gtg	gtc	atc	ttc	ctg	ggc	tcc	ttc	tac	ctg	1209		
132	Phe	Val	Phe	Phe	Val	Val	Val	Ile	Phe	Leu	Gly	Ser	Phe	Tyr	Leu			
133																385		
135	ctt	aac	cta	acc	ctg	gct	gtt	gtc	acc	atg	gct	tat	gaa	gaa	cag	aac	1257	
136	Leu	Asn	Leu	Thr	Leu	Ala	Val	Val	Thr	Met	Ala	Tyr	Glu	Glu	Gln	Asn		
137																385		
139	aga	aat	gta	gct	gct	gag	aca	gag	gcc	aag	gag	aaa	atg	ttt	cag	gaa	1305	
140	Arg	Asn	Val	Ala	Ala	Glu	Thr	Glu	Ala	Lys	Glu	Lys	Met	Phe	Gln	Glu		
141																400		
143	gcc	cag	cag	ctg	tta	agg	gag	gag	aag	gag	gct	ctg	gtt	gcc	atg	gga	1353	
144	Ala	Gln	Gln	Leu	Leu	Arg	Glu	Glu	Lys	Glu	Ala	Lys	Met	Val	Ala	Met	Gly	
145																400		
147	att	gac	aga	agt	tcc	ctt	aat	tcc	ctt	caa	gct	tca	tcc	ttt	tcc	ccg	1401	
148	Ile	Asp	Arg	Ser	Ser	Leu	Asn	Ser	Leu	Gln	Ala	Ser	Ser	Phe	Ser	Pro		
149																450		
151	aag	aag	agg	aag	ttt	ttc	ggt	agt	aag	aca	aga	aag	tcc	ttc	ttt	atg	1449	
152	Lys	Lys	Arg	Lys	Phe	Phe	Gly	Ser	Lys	Thr	Arg	Lys	Ser	Phe	Phe	Met		
153																450		
155	aga	ggg	tcc	aag	acg	gcc	caa	gcc	tca	gcg	tct	gat	tca	gag	gac	gat	1497	
156	Arg	Gly	Ser	Lys	Thr	Ala	Gln	Ala	Ser	Ala	Ser	Asp	Ser	Glu	Asp	Asp		
157																450		
159	gcc	tct	aaa	aat	cca	cag	ctc	ttt	gag	cag	acc	aaa	cga	ctg	tcc	cag	1545	
160	Ala	Ser	Lys	Asn	Pro	Gln	Leu	Leu	Glu	Gln	Thr	Lys	Arg	Leu	Ser	Gln		
161																450		
163	aac	ttg	cca	gtg	gat	ctc	ttt	gat	gag	cac	gtg	gac	ccc	ctc	cac	agg	1593	
164	Asn	Leu	Pro	Val	Asp	Leu	Phe	Asp	Glu	His	Val	Asp	Pro	Leu	His	Arg		
165																450		
167	cag	aga	gca	ctg	agc	gct	gtc	agt	atc	tta	acc	atc	acc	atg	cag	gaa	1641	
168	Gln	Arg	Ala	Leu	Ser	Ala	Val	Ser	Ile	Leu	Thr	Ile	Thr	Met	Gln	Glu		
169																450		
171	caa	gaa	aaa	ttc	cag	gag	cct	tgt	ttc	cca	tgt	ggg	aaa	aat	ttg	gcc	1689	
172	Gln	Glu	Lys	Phe	Gln	Glu	Pro	Cys	Phe	Pro	Cys	Gly	Lys	Asn	Leu	Ala		
173																450		
175	tct	aag	tac	ctg	gtg	tgg	gac	tgt	agc	cct	cag	tgg	ctg	tgc	ata	aag	1737	
176	Ser	Lys	Tyr	Leu	Val	Trp	Asp	Cys	Ser	Pro	Gln	Trp	Leu	Cys	Ile	Lys		
177																450		
179	aag	gtc	ctg	cg	acc	atc	atg	acg	gat	ccc	ttt	act	gag	ctg	gcc	atc	1785	
180	Lys	Val	Leu	Arg	Thr	Ile	Met	Thr	Asp	Pro	Phe	Thr	Glu	Leu	Ala	Ile		
181																450		
183	acc	atc	tgc	atc	atc	aat	acc	gtt	ttc	tta	gcc	gtg	gag	cac	cac		1833	
184	Thr	Ile	Cys	Ile	Ile	Ile	Asn	Thr	Val	Phe	Leu	Ala	Val	Glu	His	His		
185																450		
187	aac	atg	gat	gac	aac	tta	aag	acc	ata	ctg	aaa	ata	gga	aac	tgg	gtt	1881	
188	Asn	Met	Asp	Asp	Asn	Leu	Lys	Thr	Ile	Leu	Lys	Ile	Gly	Asn	Trp	Val		
189																450		
191	ttc	acg	gga	att	ttc	ata	gct	gaa	atg	tgt	ctc	aag	atc	atc	gct		1929	
192	Phe	Thr	Gly	Ile	Phe	Ile	Ala	Glu	Met	Cys	Leu	Lys	Ile	Ile	Ala	Leu		
193																450		

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195 gac cct tac cac tac ttc cgg cac ggc tgg aat gtt ttt gac agc atc	1976
196 Asp Pro Tyr His Tyr Phe Arg His Gly Trp Asn Val Phe Asp Ser Ile	
197 630 635 640	
199 gtg gcc ctc ctg agt ctc gct gat gtg ctc tac aac aca ctg tct gat	2025
200 Val Ala Leu Leu Ser Leu Ala Asp Val Leu Tyr Asn Thr Leu Ser Asp	
201 645 650 655	
203 aac aat agg tct ttc ttg gct tcc ctg aga gtg ctg agg gtc ttc aag	2073
204 Asn Asn Arg Ser Phe Leu Ala Ser Leu Arg Val Leu Arg Val Phe Lys	
205 660 665 670	
207 tta gcc aaa tcc tgg ccc acg tta aac act ctc att aag atc atc ggc	2121
208 Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile Gly	
209 675 680 685 690	
211 cac tcc gtg ggc gcg ctt gga aac ctg act gtg gtc ctg act atc gtg	2169
212 His Ser Val Gly Ala Leu Gly Asn Leu Thr Val Val Leu Thr Ile Val	
213 695 700 705	
215 gtc ttc atc ttt tct gtg gtg ggc atg cgg ctc ttc ggc acc aag ttt	2217
216 Val Phe Ile Phe Ser Val Val Gly Met Arg Leu Phe Gly Thr Lys Phe	
217 710 715 720	
219 aac aag acc gcc tac gcc acc cag gag cgg ccc agg cgg cgc tgg cac	2265
220 Asn Lys Thr Ala Tyr Ala Thr Gln Glu Arg Pro Arg Arg Arg Trp His	
221 725 730 735	
223 atg gat aat ttc tac cac tcc ttc ctg gtg gtg ttc cgc atc ctc tgt	2313
224 Met Asp Asn Phe Tyr His Ser Phe Leu Val Val Phe Arg Ile Leu Cys	
225 740 745 750	
227 ggg gaa tgg atc gag aac atg tgg ggc tgc atg cag gat atg gac ggc	2361
228 Gly Glu Trp Ile Glu Asn Met Trp Gly Cys Met Gln Asp Met Asp Gly	
229 755 760 765 770	
231 tcc ccg ttg tgc atc att gtc ttt gtc ctg ata atg gtg atc ggg aag	2409
232 Ser Pro Leu Cys Ile Ile Val Phe Val Leu Ile Met Val Ile Gly Lys	
233 775 780 785	
235 ctt gtg gtg ctt aac ctc ttc att gcc ttg ctg ctc aat tcc ttc agc	2457
236 Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser	
237 790 795 800	
239 aat gag gag aag gat ggg agc ctg gaa gga gag acc agg aaa acc aaa	2505
240 Asn Glu Glu Lys Asp Gly Ser Leu Glu Gly Glu Thr Arg Lys Thr Lys	
241 805 810 815	
243 gtg cag cta gcc ctg gat cgg ttc cgc cgg gcc ttc tcc ttc atg ctg	2553
244 Val Gln Leu Ala Leu Asp Arg Phe Arg Arg Ala Phe Ser Phe Met Leu	
245 820 825 830	
247 cac gct ctt cag agt ttt tgt tgc aag aaa tgc agg agg aaa aac tcg	2601
248 His Ala Leu Gln Ser Phe Cys Cys Lys Lys Cys Arg Arg Lys Asn Ser	
249 835 840 845 850	
251 cca aag cca aaa gag aca aca gaa agc ttt gct ggt gag aat aaa gac	2649
252 Pro Lys Pro Lys Glu Thr Thr Glu Ser Phe Ala Gly Glu Asn Lys Asp	
253 855 860 865	
255 tca atc ctc ccg gat gcg agg ccc tgg aag gag tat gat aca gac atg	2697
256 Ser Ile Leu Pro Asp Ala Arg Pro Trp Lys Glu Tyr Asp Thr Asp Met	
257 870 875 880	
259 gct ttg tac act gga cag gcc ggg gct ccg ctg gcc cca ctc gca gag	2745

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260	Ala	Leu	Tyr	Thr	Gly	Gln	Ala	Gly	Ala	Pro	Leu	Ala	Pro	Leu	Ala	Glu	
261	885				890										895		
263	gta	gag	gac	gat	gtg	gaa	tat	tgt	ggt	gaa	ggc	ggt	gcc	cta	ccc	acc	2793
264	Val	Glu	Asp	Asp	Val	Glu	Tyr	Cys	Gly	Glu	Gly	Gly	Ala	Leu	Pro	Thr	
265	900				905										910		
267	tca	caa	cat	agt	gct	gga	gtt	cag	gcc	ggt	gac	ctc	cct	cca	gag	acc	2841
268	Ser	Glr.	His	Ser	Ala	Gly	Val	Gln	Ala	Gly	Asp	Leu	Pro	Pro	Gln	Thr	
269	915				920										925	930	
271	aag	cag	ctc	act	agc	ccg	gat	gac	caa	ggg	gtt	gaa	atg	gaa	gta	ttt	2889
272	Lys	Gln	Leu	Thr	Ser	Pro	Asp	Asp	Gln	Gly	Val	Glu	Met	Glu	Val	Phe	
273															940	945	
275	tct	gaa	gaa	gat	ctg	cat	tta	agc	ata	cag	agt	cct	cga	aag	aag	tct	2937
276	Ser	Glu	Glu	Asp	Leu	His	Leu	Ser	Ile	Gln	Ser	Pro	Arg	Lys	Lys	Ser	
277															955	960	
279	gac	gca	gtg	agc	atg	ctc	tcg	gaa	tgc	agc	aca	att	gac	ctg	aat	gat	2985
280	Asp	Ala	Val	Ser	Met	Leu	Ser	Glu	Cys	Ser	Thr	Ile	Asp	Leu	Asn	Asp	
281															970	975	
283	atc	ttt	aga	aat	tta	cag	aaa	aca	gtt	tcc	ccc	aaa	aag	cag	cca	gat	3033
284	Ile	Phe	Arg	Asn	Leu	Gln	Ilys	Thr	Val	Ser	Pro	Lys	Lys	Gln	Pro	Asp	
285															985	990	
287	aga	tgc	ttt	ccc	aag	ggc	ctt	agt	tgt	cac	ttt	cta	tgc	cac	aaa		3078
288	Arg	Cys	Phe	Pro	Lys	Gly	Leu	Ser	Cys	His	Phe	Leu	Cys	His	Lys		
289	995						1000								1005		
291	aca	gac	aag	aga	aag	tcc	ccc	tgg	gtc	ctg	tgg	tgg	aac	att	cg		3123
292	Thr	Asp	Lys	Arg	Lys	Ser	Pro	Trp	Val	Leu	Trp	Trp	Asn	Ile	Arg		
293	1010						1015								1020		
295	aaa	acc	tgc	tac	caa	atc	gtg	aag	cac	agc	tgg	ttt	gag	agt	ttc		3168
296	Lys	Thr	Cys	Tyr	Gln	Ile	Val	Lys	His	Ser	Trp	Phe	Glu	Ser	Phe		
297	1025						1030								1035		
299	ata	atc	ttt	gtt	att	ctg	ctg	agc	agt	gga	gcg	ctg	ata	ttt	gaa		3213
300	Ile	Ile	Phe	Val	Ile	Leu	Leu	Ser	Ser	Gly	Ala	Leu	Ile	Phe	Glu		
301	1040						1045								1050		
303	gat	gtc	aat	ctc	ccc	agc	cg	ccc	caa	gtt	gag	aaa	tta	cta	agg		3258
304	Asp	Val	Asn	Leu	Pro	Ser	Arg	Pro	Gln	Val	Glu	Lys	Leu	Leu	Arg		
305	1055						1060								1065		
307	tgt	acc	gat	aat	att	ttc	aca	ttt	att	ttc	ctc	ctg	gaa	atg	atc		3303
308	Cys	Thr	Asp	Asn	Ile	Phe	Thr	Phe	Ile	Phe	Leu	Leu	Glu	Met	Ile		
309	1070						1075								1080		
311	ctg	aag	tgg	gtg	gcc	ttt	gga	tcc	cg	agg	tat	ttc	acc	agt	gcc		3348
312	Leu	Lys	Trp	Val	Ala	Phe	Gly	Phe	Arg	Arg	Tyr	Phe	Thr	Ser	Ala		
313	1085						1090								1095		
315	tgg	tgc	tgg	ctt	gat	ttc	ctc	att	gtg	gtg	gtg	tct	gtg	ctc	agt		3393
316	Trp	Cys	Trp	Leu	Asp	Phe	Leu	Ile	Val	Val	Val	Ser	Val	Leu	Ser		
317	1100						1105								1110		
319	ctc	atg	aat	cta	cca	agc	ttg	aag	tcc	ttc	cg	act	ctg	cg	gcc		3438
320	Leu	Met	Asn	Leu	Pro	Ser	Leu	Lys	Ser	Phe	Arg	Thr	Leu	Arg	Ala		
321	1115						1120								1125		
323	ctg	aga	cct	ctg	cg	g	ctg	tcc	cag	ttt	gaa	gga	atg	aag	gtt		3483
324	Leu	Arg	Pro	Leu	Arg	Ala	Leu	Ser	Gln	Phe	Glu	Gly	Met	Lys	Val		

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 5804

**VERIFICATION SUMMARY**

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:2429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:5803